

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 26.8605 Seconds

(Without alignments)  
843.812 Million cell updates/sec

Title: US-09-622-613b-24

Perfect score: 601

Sequence: 1 SMNATFOOKHIIPTICNT.....ICVKCENQYVHAGIGRCP 110

Scoring table: BLCSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_21:\*

1: sp.\_archaea:\*

2: sp.\_bacteria:\*

3: sp.\_fungi:\*

4: sp.\_human:\*

5: sp.\_invertebrate:\*

6: sp.\_mammal:\*

7: sp.\_mhc:\*

8: sp.\_organelle:\*

9: sp.\_phage:\*

10: sp.\_plant:\*

11: sp.\_rodent:\*

12: sp.\_virus:\*

13: sp.\_vertebrate:\*

14: sp.\_unclassified:\*

15: sp.\_viral:\*

16: sp.\_bacteriophage:\*

17: sp.\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586.5	97.6	133	13	09PWR7 rana catesb
2	555.5	92.4	133	13	09PWR7 rana catesb
3	482.5	80.3	132	13	09PWR7 rana catesb
4	473.5	78.8	133	13	09PWR7 rana catesb
5	466.5	77.6	133	13	09PWR7 rana catesb
6	443.5	73.8	132	13	09PWR7 rana catesb
7	371	61.7	132	13	09PWR7 rana catesb
8	276.5	46.0	127	13	09PWR7 rana catesb
9	272.5	45.3	127	13	09PWR7 rana catesb
10	241	40.1	129	13	09PWR7 rana catesb
11	224.5	37.4	128	13	09PWR7 rana catesb
12	221.5	36.9	128	13	09PWR7 rana catesb
13	212.5	35.4	128	13	09PWR7 rana catesb
14	158	26.3	128	13	09PWR7 rana catesb
15	131	21.8	170	6	09PWR7 rana catesb
16	126	21.0	150	11	09PWR7 rana catesb

17	125.5	20.9	163	6	09PWR7 rana catesb
18	124.5	20.7	116	6	09PWR7 rana catesb
19	124	20.6	150	11	09PWR7 rana catesb
20	122.5	20.4	144	6	09PWR7 rana catesb
21	120	20.0	150	11	09PWR7 rana catesb
22	116.5	19.4	152	11	09PWR7 rana catesb
23	115.5	19.2	119	6	09PWR7 rana catesb
24	114.5	19.1	124	6	09PWR7 rana catesb
25	112.5	18.7	149	11	09PWR7 rana catesb
26	112	18.6	134	6	09PWR7 rana catesb
27	111.5	18.6	152	11	09PWR7 rana catesb
28	111.5	18.6	156	6	09PWR7 rana catesb
29	110.5	18.4	119	6	09PWR7 rana catesb
30	110.5	18.4	119	6	09PWR7 rana catesb
31	110.5	18.4	124	6	09PWR7 rana catesb
32	109.5	18.2	142	6	09PWR7 rana catesb
33	109.5	18.2	156	6	09PWR7 rana catesb
34	109	18.1	124	6	09PWR7 rana catesb
35	108.5	18.1	156	6	09PWR7 rana catesb
36	108.5	18.1	156	6	09PWR7 rana catesb
37	107.5	17.9	152	11	09PWR7 rana catesb
38	106.5	17.7	149	11	09PWR7 rana catesb
39	106.5	17.7	149	11	09PWR7 rana catesb
40	105.5	17.6	116	6	09PWR7 rana catesb
41	105.5	17.6	119	6	09PWR7 rana catesb
42	105.5	17.6	157	11	09PWR7 rana catesb
43	105	17.5	158	6	09PWR7 rana catesb
44	104.5	17.4	119	6	09PWR7 rana catesb
45	104.5	17.4	124	6	09PWR7 rana catesb

## ALIGNMENTS

RESULT 1	Q9PWR7	PRELIMINARY:	PRT:	133 AA.
AC	Q9PWR7	Q9PWR7		
DT	01-MAY-2000 (TREMREL. 13, Created)			
DT	01-MAY-2000 (TREMREL. 13, Last sequence update)			
DT	01-DEC-2001 (TREMREL. 19, Last annotation update)			
DE	Ribonuclease precursor.			
GN	RCR.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
FX	MEDLINE=98165825; PubMed=9497370;			
RA	Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.,			
RT	"The Rana catesbeiana rcr gene encoding a cytoxic ribonuclease.			
RT	Tissue distribution, cloning, purification, cytotoxicity, and active			
RT	residues for RNase activity."			
RL	J. Biol. Chem. 273:6395-6401(1998).			
DR	EMBL: AF039104; AAD10702.1;			
DR	HSSP: P11916; 18C4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	PRODOM: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_PC; 1.			
DR	PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL			
FT	CHAIN			
SO	SEQUENCE			
Query Match	97.6%	Score 586.5	DB 13	Length 133;
Best Local Similarity	99.1%	Pred. No. 2.7e-60		
Matches 109;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	2	NMATFOOKHIIPTICNTIMDNNIYVGGCKRVNTEIISATVAKITGVIMNVL	60	

Db 24 NMAFFOQKHINTPILNCNTIMDNNTIYVGQCKRVNFTFISSATTVKAITGVINMVL 83  
 OY 61 STTRFOLNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFAGIGRCP 110  
 Db 84 STTRFOLNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFAGIGRCP 133

## RESULT 2

O98SMO PRELIMINARY: PRT: 133 AA.

AC O98SMO: 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE RNase A-type ribonuclease rc208 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;

SEQUENCE FROM N.A.  
 RA MEDLINE=21539506; PubMed=11683320;

RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351209; AAK30255.1; -.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; rnasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM0092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.

KW SIGNAL.  
 FT SIGNAL.

SEQUENCE 133 AA: 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.4%; Score 555.5; DB 13; Length 133;  
 Best Local Similarity 94.5%; Pred. No. 1.le-56;  
 Matches 104; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 2 NMAFFOQKHINTPILNCNTIMDNNTIYVGQCKRVNFTFISSATTVKAITGVINMVL 60  
 Db 24 NMAFFOQKHINTPILNCNTIMDNNTIYVGQCKRVNFTFISSATTVKAITGVINMVL 83  
 OY 61 STTRFOLNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFAGIGRCP 110  
 Db 84 STTRFOLNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFAGIGRCP 133

## RESULT 3

O98SMO PRELIMINARY: PRT: 132 AA.

AC O98SMO: 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;

SEQUENCE FROM N.A.  
 RA MEDLINE=21539506; PubMed=11683320;

RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351209; AAK30255.1; -.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; rnasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM0092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW SIGNAL.  
 FT SIGNAL.

SEQUENCE FROM N.A.  
 RA MEDLINE=21539506; PubMed=11683320;

RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351209; AAK30255.1; -.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.

RA Liao Y.-D., Tang P.-C., Jeng J.-T.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF351207; AAK30253.1; -.  
 DR EMBL: AF359578; AAL87036.1; -.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM0092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.

KW SIGNAL.  
 FT SIGNAL.  
 FT CHAIN  
 SQ SEQUENCE 132 AA: 14412 MW; 131A745187978687 CRC64;

Query Match 80.3%; Score 482.5; DB 13; Length 132;  
 Best Local Similarity 84.3%; Pred. No. 3e-48;  
 Matches 91; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

OY 3 NMAFFOQKHINTPILNCNTIMDNNTIYVGQCKRVNFTFISSATTVKAITGVINMVL 61  
 Db 25 NMAFFOQKHINTPILNCNTIMDNNTIYVGQCKRVNFTFISSATTVKAITGVINMVL 84  
 OY 62 STTRFOLNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFAGIGRCP 109  
 Db 85 STTRFOLNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFAGIGRCP 132

## RESULT 4

O98SL9 PRELIMINARY: PRT: 133 AA.

AC O98SL9: 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE RNase A-type ribonuclease rc212 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;

SEQUENCE FROM N.A.  
 RA MEDLINE=21539506; PubMed=11683320;

RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351210; AAK30256.1; -.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; rnasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM0092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.

KW SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 133 AA: 14615 MW; C878B236B2654E CRC64;

Query Match 78.8%; Score 473.5; DB 13; Length 133;  
 Best Local Similarity 78.2%; Pred. No. 3.4e-47;  
 Matches 86; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

OY 2 NMAFFOQKHINTPILNCNTIMDNNTIYVGQCKRVNFTFISSATTVKAITGVINMVL 60  
 Db 24 NMAFFOQKHINTPILNCNTIMDNNTIYVGQCKRVNFTFISSATTVKAITGVINMVL 83

OY 61 STTRFOLNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFAGIGRCP 110  
 Db 84 STTRFOLNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFAGIGRCP 133

## RESULT 5

O98SL8

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ID 098SL8 PRELIMINARY: PRT: 133 AA.
AC 098SL8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc213 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351211; AAK30257.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_PC.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A4FA5B943 CRC64;

Query Match 77.68; Score 466.5; DB 13; Length 133;
Best Local Similarity 76.48; Pred. No. 2.2e-46;
Matches 84; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

QY 2 NMATPOOKHIINPIL-CNTIMDNINIIYVGQCKRVNFTFIISATYKATCTGVINNVL 60
DB 24 NMATPOOKHIINPIL-CNTIMDNINIIYVGQCKRVNFTFIISATYKATCTGVINNVL 83
QY 61 STTRPOLNCTRTSTIRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 110
DB 84 STTRPOLNCTRTSTIRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 133

RESULT 6
Q98SM1 PRELIMINARY: PRT: 132 AA.
AC 098SM1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351208; AAK30254.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_PC.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 73.88; Score 443.5; DB 13; Length 132;
Best Local Similarity 78.08; Pred. No. 1e-43;

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Matches 85; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 2 NMATPOOKHIINPIL-CNTIMDNINIIYVGQCKRVNFTFIISATYKATCTGVINNVL 60
DB 24 NMATPOOKHIINPIL-CNTIMDNINIIYVGQCKRVNFTFIISATYKATCTGVINNVL 83
QY 61 STTRPOLNCTRTSTIRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 109
DB 84 STTRPOLNCTRTSTIRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 132

RESULT 7
Q9DF78 PRELIMINARY: PRT: 132 AA.
AC 09DF78;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RC-Nase1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF288642; AAC30414.2; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_PC.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;

Query Match 61.78; Score 371; DB 13; Length 132;
Best Local Similarity 65.58; Pred. No. 2.6e-35;
Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 NMATPOOKHIINPIL-CNTIMDNINIIYVGQCKRVNFTFIISATYKATCTGVINNVL 59
DB 23 NMATPOOKHIINPIL-CNTIMDNINIIYVGQCKRVNFTFIISATYKATCTGVINNVL 82
QY 60 LSTRPOLNCTRTSTIRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 109
DB 83 LSTRPOLNCTRTSTIRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 132

RESULT 8
Q918V8 PRELIMINARY: PRT: 127 AA.
AC 0918V8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Onconase variant rapiri precursor.
OS Rana pipiens (Northern Leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;

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RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF159166; AAD41901.1; -  
 DR HSSP: P00656; ILSO.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 SQ SEQUENCE 169 AA; 18891 MW; D969FE43B3CE1B8 CRC64;

Query Match 26.3%; Score 158; DB 13; Length 169;  
 Best Local Similarity 38.7%; Pred. No. 1.7e-10;

Matches 43; Conservative 10; Mismatches 50; Indels 8; Gaps 6;

OY 2 NMATFOCKHII--NTPICN-TIMDNNIYVIGOCKRVNFTI-ISSATTVKAICTGVIM 57  
 DB 29 NINAFMEKHIVKEAEINCNQITIKDRIIRF-KNNCKFRNFTIHDTNGKKYKMGAGIYKS 87  
 OY 58 N-VLSTRTFOLNCTRTSTPRP--CPYSSRTETNYICVGCENQYPVHFAG 105  
 DB 88 TFVISKELPLTJDCLLMGRTARPPNCAYNQTRTGTGINITCENNYPVHFAG 138

## RESULT 15

O9BEC1 ID O9BEC1 PRELIMINARY; PRT; 170 AA.

AC O9BEC1;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Brain-type ribonuclease ribonuclease precursor (Fragment).  
 GN RNase B.  
 OS Tragus javanicus (Lesser Malay chevrotain).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;  
 OC Tragulidae; Tragulus.  
 OX NCBI\_TaxID=9849;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21347458; Pubmed-11453981;  
 RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,  
 RA Wamelis H.W., Beintema J.J.;  
 RT "Secretory ribonucleases in the primitive ruminant chevrotain  
 (Tragus javanicus).";  
 RL Eur. J. Biochem. 268:3890-3897(2001).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR EMBL: AJ271299; CAC24723.1; -  
 DR HSSP: P00656; ILSO.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KW Endonuclease; Hydrolase; Nuclease; Signal.  
 FT CON\_TER 1  
 FT SIGNAL <1 19  
 FT CHAIN 20 170  
 SQ SEQUENCE 170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;

Query Match 21.8%; Score 131; DB 6; Length 170;  
 Best Local Similarity 33.1%; Pred. No. 2.3e-07;

Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;

OY 4 ATFOQKHII-----INPIICNTIMDNNIYVIGOCKRVNFTIISATTVKAICT----- 52  
 DB 25 AKFRROHLDAAGNSSINSN-YCNLMKRR-KMTHGRCKRPVNTFIHESLEDAVKAICSEKNIT 82  
 OY 53 ---GVIMNVLTSTRTFOLNCTRTSTPRP--CPYSSRTETNYICVGCEN--QYVHFAGI 106  
 DB 83 CKNGQPMCHOSNST-MNITDCRGTGSGSKYPNCAIKTSOKOKYIIVACEGTPSVPHFDGS 141  
 OY 107 GRCP 110

DB 142 AVLP 145

Search completed: June 25, 2003, 14:55:26  
 Job time : 26.9438 secs